retinal_blastoma

2022-09-28

Step 1: Install package

##already installed

```
#devtools::install_github('progenetix/pgxRpi')
library(pgxRpi)
```

Step2: Search retinal blastoma (NCIT:C7541)

```
freq <- pgxLoader(type='frequency', output='pgxseg',filters='NCIT:C7541',
                  codematches=T) #only want this specific cancer so use codematches=T
```

Step3: Access the CNV frequency data from samples with

The retreived data is an object contaning two slots `meta` and `data`.

```
freq$meta
```

```
##         code          label sample_count
## 1 NCIT:C7541 Retinoblastoma          173
## 2      total                       173
```

```
names(freq$data)
```

```
## [1] "NCIT:C7541" "total"
```

```
head(freq$data$`NCIT:C7541`)
```

```
##      filters reference_name   start     end gain_frequency loss_frequency no
## 1 NCIT:C7541              1       0  400000          2.312          4.624  1
## 2 NCIT:C7541              1  400000 1400000          2.312          5.202  2
## 3 NCIT:C7541              1 1400000 2400000          2.312          5.202  3
## 4 NCIT:C7541              1 2400000 3400000          2.312          5.780  4
## 5 NCIT:C7541              1 3400000 4400000          2.312          5.780  5
## 6 NCIT:C7541              1 4400000 5400000          2.312          5.780  6
```

Dimension of this matrix

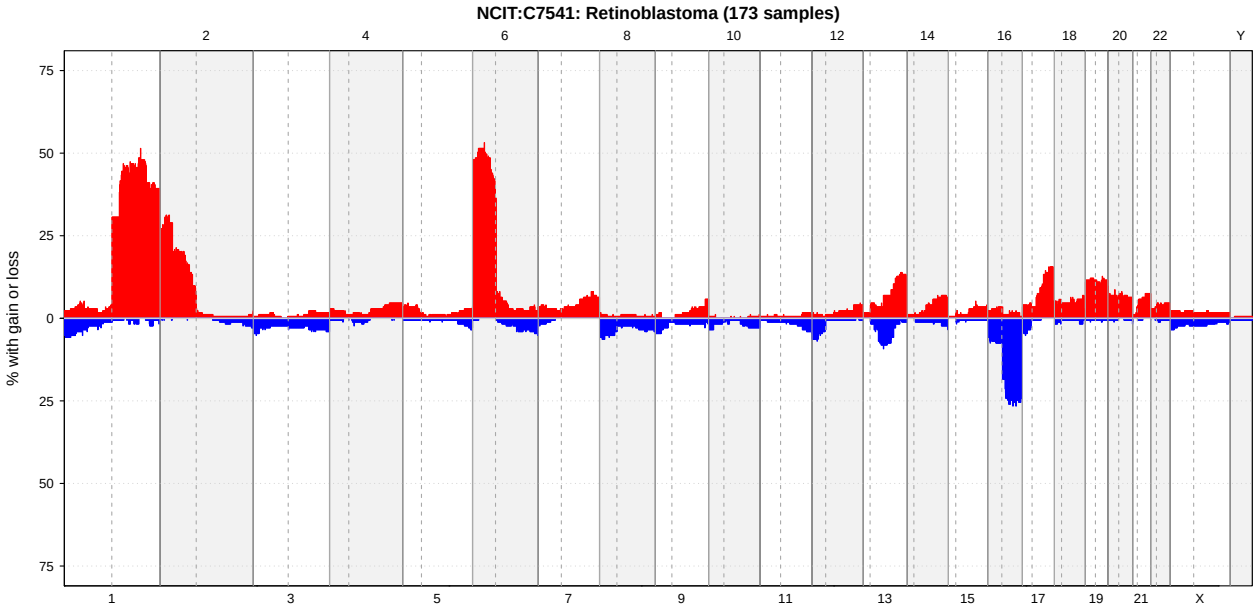
```
dim(freq$data$`NCIT:C4025`) #dimensions
```

```
## NULL
```

Step4: Visualize data

By genome

```
pgxFreqplot(freq)
```



Step5: Analyse the data

According the plot, we can see frequenct gains on chromosome 1q, 6p #and frequenct losses on chromosome 16q